

# SEQUENCE LISTING

<110> Cahoon, Rebecca E.  
Fang, Yiwen  
Odell, Joan  
Weng, Zude

<120> Plant Myb Transcription Factor Homologs

<130> BB1294 US NA

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<150> 60/110,609  
<151> 1998-December-02

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 cgcaaggggc cgtggacgct ggaggaggac ctcatcctcg tcagctacat ctcccagcac 180  
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 Val Ser Tyr Ile Ser Gln His Gly Glu Gly Ser Trp Asp Asn Leu Ala  
 35 40 45  
 Arg Ala Ala Gly Leu Asn Arg Asn Gly Lys Ser Cys Arg Leu Arg Trp  
 50 55 60  
 Leu Asn Tyr Leu Arg Pro Gly Val Arg Arg Gly Ser Ile Thr Ala Gly  
 65 70 75 80  
 Glu Asp Thr Val Ile Arg Glu Leu His Ala Arg Trp Gly Asn Lys Trp  
 85 90 95  
 Ser Lys Ile Ser Lys His Leu Pro Gly Arg Thr Asp Asn Glu Xaa Lys  
 100 105 110  
 Asn Tyr Trp Arg Thr Arg Ile Gln Gln Glu Glu Gln Gln Gly Ala Lys  
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 cggctcccag ccgatacaag gtaggagtga gcagcgttag ttatcatcata tcgcataggc 240  
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Trp Asp Phe Ile Ala Lys Val Ser Gly Leu Asn Arg Thr Gly Lys Ser  
35 40 45  
Cys Arg Leu Arg Trp Val Asn Tyr Leu His Pro Gly Leu Lys Arg Gly  
50 55 60  
Arg Met Ser Pro His Glu Glu Arg Leu Ile Leu Glu Leu His Ala Arg  
65 70 75 80  
Trp Gly Asn Arg Trp Ser Arg Ile Ala Arg Arg Leu Pro Gly Arg Thr  
85 90 95  
Asp Asn Glu Ile Lys Asn Tyr Trp Arg Thr His Met Arg Lys Lys Ala  
100 105 110  
Gln Glu Arg Lys Arg Asn Met Ser Pro Ser Ser Ser Ser Ser Leu  
115 120 125  
Ser Tyr Gln Ser Gly Tyr Pro Asp Thr Pro Ser Ile Ile Gly Val Lys  
130 135 140  
Gly Gln Glu Leu His Gly Gly Ser Gly Cys Ile Thr Ser Ile Leu Lys  
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Glu Leu Lys

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ggcgcggtgac caccgagagc tgagcggcga cgaggactcc gtggtggcgg ccggagacct 180

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          20          25          30
Met Leu Leu Val Asn Tyr Val Ala Ala His Gly Glu Gly Arg Trp Asn
          35          40          45
Ala Leu Ala Arg Cys Ala Gly Leu Arg Arg Thr Gly Lys Ser Cys Arg
          50          55          60
Leu Arg Trp Leu Asn Tyr Leu Arg Pro Asp Leu Arg Arg Gly Asn Ile
          65          70          75          80
Thr Ala Gln Glu Gln Leu Leu Ile Leu Glu Leu His Ser Arg Trp Gly
          85          90          95
Asn Arg Trp Ser Xaa Ile Ala Gln His Leu Gln Gly Gln Arg Gln Arg
          100          105          110
Xaa Xaa Asn Tyr Trp Arg Thr Gly
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 Ala Ala Gly Leu Lys Arg Thr Gly Lys Xaa Cys Arg Leu Arg Trp Xaa  
 35 40 45  
 Asn Tyr Leu Arg Pro Asp Val Lys Arg Gly Asn Phe Ser Ala Asp Glu  
 50 55 60  
 Gln Leu Leu Ile Ser Thr Ser His  
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 20          25          30

His His Ser His Gln Leu Lys Gly Gly Ala Gln Glu Glu Ala Glu Asn
 35          40          45

Asp Asn Asn Lys Pro Glu Leu Arg Arg Gly Pro Trp Thr Val Asp Glu
 50          55          60

Asp Leu Thr Leu Val Asn Tyr Ile Ala Asp Asn Gly Glu Gly Arg Trp
 65          70          75          80

Asn Asn Leu Ala Arg Ala Ala Gly Leu Lys Arg Thr Gly Lys Ser Cys
 85          90          95

Arg Leu Arg Trp Leu Asn Tyr Leu Arg Pro Asp Val Lys Arg Gly Asn
100         105         110

Phe Ser Ala Asp Glu Gln Leu Leu Ile Leu Asp Leu His Thr Arg Trp
115         120         125

Gly Asn Arg Trp Ser Lys Ile Ala Gln His Leu Pro Gly Arg Thr Asp
130         135         140

Asn Glu Ile Lys Asn Tyr Trp Arg Thr Arg Val Gln Lys His Ala Lys
145         150         155         160

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Gln Leu Asn Cys Asp Ala Asn Ser Lys Arg Phe Lys Asp Ala Met Arg  
165 170 175

Tyr Leu Trp Met Pro His Leu Ala Asp Asp Val Asp Thr Ile Ala Ala  
180 185 190

Ala Asn Asp Asp Asp Glu Asp His His His Asn Leu Arg Leu Leu Val  
195 200 205

Leu His His His Gln Ala Gln His Leu Gln Gln Ala Ala Ala Ala Ala  
210 215 220

Gly Gly Ala Ala Asn Asp Leu Ala Ala Gly Ala Tyr Asp Val Arg Gln  
225 230 235 240

Leu His Ala Leu Pro Ser Ser Gly Met Ala Ala Thr Ser Ser Ser Asp  
245 250 255

Ser Leu Ala Ser Glu Ser Tyr Asp Asp Gly Gly Leu Leu Phe Ala Asn  
260 265 270

Leu Arg Ala Gly Glu Met Leu Met Asp Gly Gly Asp Trp Ala Ala Gln  
275 280 285

Gln Glu Ala Asp Gln Gly Leu Trp Pro Pro Pro Pro Pro Pro Ser  
290 295 300

Asp Leu Asp Gln Ser Val Val Gln Ala Ala Gly Ala Gly Ala Gly Gln  
305 310 315 320

Phe Gln Asp Met Glu Leu Ser Gly Trp Val Gln Gly Phe Ser Glu Ser  
325 330 335

Ile Thr Asp Asn Phe Trp Ala Leu Glu Glu Ile Trp Lys Met Gln  
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atgtcgatca gatggatgga tgcattcata tgccgtacat agtagatttg atgatagtaa 180  
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atggtggtgc agctccacgc caagctcggc aacaggtggt ctgcgcatcg caagagcatt 420  
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Gly Arg Met Ser Pro Glu Glu Glu Arg Met Val Val Gln Leu His Ala  
 35 40 45

Lys Leu Gly Asn Arg Trp Ser Arg Ile Ala Lys Ser Ile Pro Gly Arg  
 50 55 60

Thr Asp Asn Glu Ile Lys Asn  
 65 70

<210> 13  
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 aggaggagga ggaataatga gaaagggccc gtggacggag caggaggacg tgcagttggt 180  
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 caacaggtgg tctgcatcg ccaagagcat tcttgccgc accgacaacg agatcaagaa 420  
 ctactggcgc acccacctgc gcaagctcaa gctcaaacag caaaagcagc agcagtccga 480  
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 aatctctgat cagtactata taaatatata tatatatgta acagctgcta gctatagcta 1080  
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 Ser Gly Leu Gln Arg Ser Gly Lys Ser Cys Arg Leu Arg Trp Val Asn  
 35 40 45  
 Tyr Leu His Pro Gly Leu Lys Arg Gly Arg Met Ser Pro Glu Glu Glu  
 50 55 60  
 Arg Met Val Val Gln Leu His Ala Lys Leu Gly Asn Arg Trp Ser Arg  
 65 70 75 80

Ile Ala Lys Ser Ile Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr  
85 90 95

Trp Arg Thr His Leu Arg Lys Leu Lys Leu Lys Gln Gln Lys Gln Gln  
100 105 110

Gln Ser Asp Asp His His Asn Asp Asn Asp Asp Asp Asp Arg Asn  
115 120 125

Ser Ser Ser Ser Ser Ser Ser Ser Asn Ser Asn Ser Asn Leu Gln Gln  
130 135 140

Gln Pro Gln Pro Glu Asp Glu Ser Ser Ala Ser Gly Ser Leu Gln Ala  
145 150 155 160

Gln His His Glu Asp Gln His Gln Leu Phe Leu His Pro Leu Trp Asn  
165 170 175

Asp Asp Ile Ile Val Asp Val Asp Cys Trp Ser Ser Ser Thr Asn Val  
180 185 190

Val Ala Pro Pro Pro Met Pro Ala Ser Pro Leu Trp Asp Ile Asp Asp  
195 200 205

Ala Phe Phe Cys Ser Asp Tyr Ser Leu Pro Leu Trp Gly  
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acatcccaag cccaatatg gtgacagtga gagaggagat gcgcaaggga ccatggacag 180  
agcaggagga cctgcaactg gtatgcactg tccgcctgtt cggtgaccgc cgttgggatt 240  
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20 25 30

Trp Asp Phe Val Ala Lys Val Ser Gly Leu Arg Gly Leu Asn Arg Thr  
 35 40 45

Gly Lys Ser Cys Arg Leu Arg Trp Val Asn Xaa Leu Gln Pro  
 50 55 60

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 cgtcaactac atcgccgccc atggcgaggg ccgctggaac gcgctcgcg cgtgcgccgg 180  
 gctgaagcgg acggggaaga gctgccggct gcggtggctg aactacctga ggccggacgt 240  
 gaggaggggg aacatgacgg cggaggagca gctgctgata ctggagctcc atgggcgggtg 300  
 ggggaatcgg tggagcaaga tcgcgagca tctccccggc cgcaccgaca acgagatcaa 360  
 gaactactgg cgcacccgcg tccagaagca cgccaagcac ctcaactgcg acgtcaactc 420  
 ccagcagttc aaggacctca tgcgctacct ctggatgccc gcctcctcga acgcatcaac 480  
 gctcctccca atccaatcca cgacccgacg acccgactct cgtctccgcc gcacactgat 540  
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<210> 18  
 <211> 145  
 <212> PRT  
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 20 25 30

Val Asn Tyr Ile Ala Ala His Gly Glu Gly Arg Trp Asn Ala Leu Ala  
 35 40 45

Arg Cys Ala Gly Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp  
 50 55 60

Leu Asn Tyr Leu Arg Pro Asp Val Arg Arg Gly Asn Met Thr Ala Glu  
 65 70 75 80

Glu Gln Leu Leu Ile Leu Glu Leu His Gly Arg Trp Gly Asn Arg Trp  
 85 90 95

Ser Lys Ile Ala Gln His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys  
100 105 110

Asn Tyr Trp Arg Thr Arg Val Gln Lys His Ala Lys His Leu Asn Cys  
115 120 125

Asp Val Asn Ser Gln Gln Phe Lys Asp Leu Met Arg Tyr Leu Trp Met  
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Pro  
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tcccgatggg gcaaccgatg gtccaagata gcacaacatt tgccctgggag gaccgacgac 180  
gagatcaaga actactggag gaccagagtg caaaagcatg ccaagcaact caattgtgat 240  
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cgcatccatg ccagggctgg cgctgttgat gatagcggag actacagcaa caacgactta 360  
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Asn Tyr Leu Arg Pro Asp Val Lys Arg Gly Asn Phe Thr Ala Glu Glu  
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Gln Leu Leu Ile Leu Asp Leu His Ser Arg Trp Gly Asn Arg Trp Ser  
35 40 45  
Lys Ile Ala Gln His Leu Pro Gly Arg Thr Asp Asp Glu Ile Lys Asn  
50 55 60  
Tyr Trp Arg Thr Arg Val Gln Lys His Ala Lys Gln Leu Asn Cys Asp  
65 70 75 80  
Val Asn Ser Lys Arg Phe Lys Asp Ala Met Lys Tyr Leu Trp Met Pro  
85 90 95  
Arg Leu Ala Glu Arg Ile His Ala Arg Ala Gly Ala Val Asp Asp Ser  
100 105 110  
Gly Asp Tyr Ser Asn Asn Asp Leu Ser Cys Val Ser Gly Val Thr Met  
115 120 125  
Ala Thr Val Ala Asn Cys Phe Asp Gly Ser Pro Ser Met Val Thr Ser  
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Ser Ser  
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tctatccgat caatcgactg gcccgcgagg atcgatcgag actcgaaagg gagggatttt 180  
gatccggatc ggtcgacgat ggacatggcg cagagagagg acgcgagcag cgaggaggag 240  
gtgatgggcg gcgacctgcg tcgcggggccg tggacgggtgg aggaggacct cctgctcgtc 300  
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aaacgcacag gcaagagctg ccggctccgg tggtgaact acctccgccc cgacctccgg 420  
cgaggcaaca tcacgccgca agagcagctg ctcatcctgg agctgcactc gcggtgggga 480  
aaccgctggt ccaagatngc gcagcacctc ccgggaagca ccgacaacga gatnaagaat 540  
acnggcgcac gcggtgcaga agcaccacaag cagtcaagtg cnactcaaca gcaacantta 600  
aggacncatg cgctactcng gatgcccgct cttnagggat 640

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 Gly Gly Asp Leu Arg Arg Gly Pro Trp Thr Val Glu Glu Asp Leu Leu  
                   20                  25                  30  
 Leu Val Asn Tyr Ile Ala Ala His Gly Glu Gly Arg Trp Asn Ser Leu  
                   35                  40                  45  
 Ala Arg Ser Ala Xaa Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg  
           50                  55                  60  
 Trp Leu Asn Tyr Leu Arg Pro Asp Leu Arg Arg Gly Asn Ile Thr Pro  
           65                  70                  75                  80  
 Gln Glu Gln Leu Leu Ile Leu Glu Leu His Ser Arg Trp Gly Asn Arg  
                   85                  90                  95  
 Trp Ser Lys Xaa Ala Gln His Leu Pro Gly Ser Thr Asp Asn Glu Xaa  
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 Lys Asn Thr  
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 gggggccatgg acgccggagg aggacctgat gctgggtctcc tacatccagg agcacggcgc 180  
 cggcaactgg cgcgccgtgc cgacgaacac cgggctgatg cgttgcagca agagctgccg 240  
 gctccgggtgg acgaactacc tcaggccggg gatcaagcgg gggaacttca ccgagcanga 300  
 ggagaagctc atcgtccacc tccaggctct cctcggcaac cgggtgggcaa cgatnncgtc 360  
 gtacttgccg gganangacg ncaacnacat cangaatact gggaacannc acctcangaa 420  
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 <212> PRT  
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Gly Ala Gly Asn Trp Arg Ala Val Pro Thr Asn Thr Gly Leu Met Arg  
 35 40 45

Cys Ser Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Gly  
 50 55 60

Ile Lys Arg Gly Asn Phe Thr Glu Xaa Glu Glu Lys Leu Ile Val His  
 65 70 75 80

Leu Gln Ala Leu Leu Gly Asn Arg Trp Ala Thr Xaa Xaa Ser Tyr Leu  
85 90 95

Pro Gly Xaa Asp Xaa Asn Xaa Ile Xaa Asn Thr Gly Asn Xaa His Leu  
100 105 110

Xaa Lys Asn Ser Arg Xaa Cys Lys Pro Pro Glu Val Xaa Lys  
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<210> 25  
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<213> Oryza sativa

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tgaagaaggg gccatggacg ccggaggagg acctgatgct ggtctcctac atccaggagc 180  
acggcgccgg caactggcgc gccgtgccga cgaacaccgg gctgatgcgt tgcagcaaga 240  
gctgccggct ccgggtggac aactacctca ggccggggat caagcggggg aacttcaccg 300  
agcaggagga gaagctcatc gtccacctcc aggtctctct cggcaaccgg tgggcagcga 360  
tagcgtcgta cttgccggag aggacggaca acgacatcaa gaactactgg aacacgcacc 420  
tcaagaagaa gctcaagaag atgcaggccg ccggagggtg ggaagacagc ggccgcgcct 480  
cggaggggtg ccggcgccgc gccgacggcg accggcgccg gaaaagcgtg aaggccgccg 540  
cacctaaggg gcagtgggag ccggcggtgc agacggacat ccacacggcg cggcaggcgc 600  
tgccgcagcg gctctcgctc gaccaccccg acccgctgcc ggccagggcg gcggcgccgg 660  
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cgccggcggt ctcgatgctg gagagctggc tgctcgacga ccggcgccatg gggctcatgg 1020  
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aagatgcaac taatcaaagc taattaaaag ggcttcgagt taattctcgg tgattttaat 1200  
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<211> 323  
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<213> Oryza sativa

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20 25 30  
Gly Ala Gly Asn Trp Arg Ala Val Pro Thr Asn Thr Gly Leu Met Arg  
35 40 45  
Cys Ser Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Gly  
50 55 60

Ile Lys Arg Gly Asn Phe Thr Glu Gln Glu Glu Lys Leu Ile Val His  
 65 70 75 80  
 Leu Gln Ala Leu Leu Gly Asn Arg Trp Ala Ala Ile Ala Ser Tyr Leu  
 85 90 95  
 Pro Glu Arg Thr Asp Asn Asp Ile Lys Asn Tyr Trp Asn Thr His Leu  
 100 105 110  
 Lys Lys Lys Leu Lys Lys Met Gln Ala Ala Gly Gly Gly Glu Asp Ser  
 115 120 125  
 Gly Ala Ala Ser Glu Gly Gly Gly Gly Arg Gly Asp Gly Asp Gly Gly  
 130 135 140  
 Gly Lys Ser Val Lys Ala Ala Ala Pro Lys Gly Gln Trp Glu Arg Arg  
 145 150 155 160  
 Leu Gln Thr Asp Ile His Thr Ala Arg Gln Ala Leu Arg Asp Ala Leu  
 165 170 175  
 Ser Leu Asp His Pro Asp Pro Ser Pro Ala Thr Ala Ala Ala Ala Ala  
 180 185 190  
 Thr Pro Ala Gly Ser Ser Ala Ala Tyr Ala Ser Ser Ala Asp Asn Ile  
 195 200 205  
 Ala Arg Leu Leu Gln Gly Trp Met Arg Pro Gly Gly Gly Gly Gly Gly  
 210 215 220  
 Asn Gly Lys Gly Pro Glu Ala Ser Gly Ser Thr Ser Thr Thr Ala Thr  
 225 230 235 240  
 Thr Gln Gln Gln Pro Gln Cys Ser Gly Glu Gly Ala Ala Ser Ala Ser  
 245 250 255  
 Ala Ser Ala Ser Gln Ser Gly Ala Ala Ala Ala Ala Thr Ala Gln Thr  
 260 265 270  
 Pro Glu Cys Ser Thr Glu Thr Ser Lys Met Ala Thr Gly Gly Gly Ala  
 275 280 285  
 Gly Gly Pro Ala Pro Ala Phe Ser Met Leu Glu Ser Trp Leu Leu Asp  
 290 295 300  
 Asp Gly Gly Met Gly Leu Met Asp Val Val Pro Leu Gly Asp Pro Ser  
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 Glu Phe Phe

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 agaagacttg atcttngatc aactatatattg caaatcatgg ggaagggtgtt tggaattctt 180

tggccaaaag ctgctgggtct caaacgtacc ggaaagattg ccggctaang tggctaaact 240  
 acctccgtcc tgatgttaga agagggaata ntacaccoga aggaacaact ttgatcatgg 300  
 agcttcacgc aaagtgggga aacagggtgg ccaaaattgc caagcatcta cctggtagga 360  
 cagtaatgag atnaagaact antggnggac aaggatcaga agcacatcaa gcaactgaga 420  
 attnagcaac aatcacataa ctctgagata atgttacaag ctagatacca agttntacaa 480  
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Leu Ile Xaa Xaa Ile Asn Tyr Ile Ala Asn His Gly Glu Gly Val Trp  
 20 25 30

Asn Ser Leu Ala Lys Ser Cys Trp Ser Gln Thr Tyr Arg Lys Asp Cys  
 35 40 45

Arg Leu Xaa Trp Leu Asn Tyr Leu Arg Pro Asp Val Arg Arg Gly Asn  
 50 55 60

Xaa Thr Pro Glu Gly Thr Thr Leu Ile Met Glu Leu His Ala Lys Trp  
 65 70 75 80

Asn Arg Trp Ser Lys Ile Ala Lys His Leu Pro Gly Arg Thr  
 85 90

<210> 29  
 <211> 988  
 <212> DNA  
 <213> Glycine max

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 acgatggaag aagacttgat cttgatcaac tatattgcaa atcatgggga aggtgtttgg 180  
 aattcttttg ccaaagctgc tgggtctcaa cgtaccggaa agagttgccg gctaagggtgg 240  
 ctaaactacc tccgtcctga tggttagaaga gggaatatta caccogagga acaacttttg 300  
 atcatggagc ttcacgcaaa gtggggaaac aggtgggtcca aaattgccaa gcatctacct 360  
 ggtaggacag ataatgagat caagaactat tggaggacca ggatccagaa gcacatcaag 420  
 caagctgaga acttttcagca acaaactcagc aataactctg agataaatga tcaccaagct 480  
 agcactagcc atgtttctac catggctgaa cccatggaga cctattctcc acccttttat 540  
 caaggaatgt tagagccatt ttcttcaatt cagttcccca caattaatcc tgatcaatcc 600

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gtttgcttaa aaaaaaaaaa aaaaaaaaaa 988

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<210> 30
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<212> PRT
<213> Glycine max

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      20          25          30

Ala Asn His Gly Glu Gly Val Trp Asn Ser Leu Ala Lys Ala Ala Gly
      35          40          45

Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu
      50          55          60

Arg Pro Asp Val Arg Arg Gly Asn Ile Thr Pro Glu Glu Gln Leu Leu
      65          70          75          80

Ile Met Glu Leu His Ala Lys Trp Gly Asn Arg Trp Ser Lys Ile Ala
      85          90          95

Lys His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Arg
      100          105          110

Thr Arg Ile Gln Lys His Ile Lys Gln Ala Glu Asn Phe Gln Gln Gln
      115          120          125

Ile Ser Asn Asn Ser Glu Ile Asn Asp His Gln Ala Ser Thr Ser His
      130          135          140

Val Ser Thr Met Ala Glu Pro Met Glu Thr Tyr Ser Pro Pro Phe Tyr
      145          150          155          160

Gln Gly Met Leu Glu Pro Phe Ser Ser Ile Gln Phe Pro Thr Ile Asn
      165          170          175

Pro Asp Gln Ser Ser Cys Cys Thr Asn Asp Asn Asn Asn Ser Ile Asn
      180          185          190

Tyr Trp Ser Met Glu Asp Ile Trp Ser Met Gln Leu Leu Asn Gly Asp
      195          200          205

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<211> 530
<212> DNA
<213> Glycine max

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 tggaaactctt tggccaaggc tgctggactt aaacgtaccg gaaagagttg ccgggtccgg 180  
 tggctaaaact acctccgtcc tgatgttaga agagggaata ttacacccga ggaacagctt 240  
 ttgatcatgg aacttcatgc aaagtgggga aacaggtggt ccaaaattgc caagcatcta 300  
 nccggaagga ctgataatga gattaagaac tactggagga caaggatcaa gaacanctca 360  
 agcaagcctt caacaacttc aacaacanag tantaattct gagataattt acatcccaag 420  
 cttgcacaac caattgtcaa caatgggcaa ccaaaaaaaaa ctaatctcan caatttcaag 480  
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 <211> 204  
 <212> PRT  
 <213> Glycine max

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Gly Pro Trp Thr Met Glu Glu Asp Leu Ile Leu Ile Thr Tyr Ile Ala  
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 Asn His Gly Glu Gly Val Trp Asn Ser Leu Ala Lys Ala Ala Gly Leu  
                     35                    40                    45  
 Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg  
                     50                    55                    60  
 Pro Asp Val Arg Arg Gly Asn Ile Thr Pro Glu Glu Gln Leu Leu Ile  
                     65                    70                    75                    80  
 Met Glu Leu His Ala Lys Trp Gly Asn Arg Trp Ser Lys Ile Ala Lys  
                     85                    90                    95  
 His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Arg Thr  
                     100                    105                    110  
 Arg Ile Gln Lys His Leu Lys Gln Ala Ser Ser Ser Phe Gln Gln Gln  
                     115                    120                    125  
 Ser Ser Asn Ser Glu Ile Ile Tyr His Pro Gln Ala Cys Thr Ser Gln  
                     130                    135                    140  
 Val Ser Thr Met Ala Gln Pro Ile Glu Thr Tyr Ser Pro Pro Ser Tyr  
                     145                    150                    155                    160  
 Gln Gly Met Leu Asp Pro Phe Ser Ile Gln Phe Pro Thr Asn Pro His  
                     165                    170                    175  
 His Ser Ser Cys Cys Thr Asn Asp Asp Asp Asn Asn Asn Tyr Trp Ser  
                     180                    185                    190  
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 aactatattg caaatcacgg tgaagtggtt tggattctt tagccaaagc ttctggtctt 180  
 aaacgaacgg gaaagagttg tcgactccgt tggctaaact accttcgtcc tgatgttaga 240  
 agaggaaaca ttacaccgga agaacagctt ttgatcatag aacttcatgc aaagtggggc 300  
 aataggtggt ccaaaattgc aaagcatctt ccaggaagaa ctgacaatga gattaagaac 360



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ttctggagaa ctaggatcca gaagcacatt aagcaagctg agacttcaca acaacatggt 420
aattcatcag agaatagtaa taatgatcat caagcaagca atagcactag caaggtgtcc 480
accatggcac atccaaatga gactttctct tcaccctcat accaagcaac ttttgagcca 540
tttcaacctc aattcctaca atcaatgata aatcaagttg ttgtaccagc aacaacaact 600
attggagcat cgaggatata tggtcgtcta tgcaattact caatggagat waattaaatc 660
tagctatatg catgcttata taaatcataat atgtgatgat atataaacct aagctcttat 720
tgagtgtggt caggcttaat aacatcatta ggtctggtat atatgagtag gttaagattg 780
gtgtgcatgc ctaaaatgnag tattgcntta ttgnagtaag aataactagt tatggatgcc 840
tttaaaaaaa agttagttaa gaattgaaat atatagtaac ttatatacta aaaaaaaaaa 900
aaaaaaaaaa                                     910

```

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<210> 34
<211> 206
<212> PRT
<213> Glycine max

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<400> 34
Met Asp Lys Lys Pro Cys Asp Ser Ser His Asp Pro Glu Val Arg Lys
 1          5          10          15

Gly Pro Trp Ile Met Glu Glu Asp Leu Ile Leu Ile Asn Tyr Ile Ala
      20          25          30

Asn His Gly Glu Gly Val Trp Asn Ser Leu Ala Lys Ala Ser Gly Leu
      35          40          45

Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg
      50          55          60

Pro Asp Val Arg Arg Gly Asn Ile Thr Pro Glu Glu Gln Leu Leu Ile
      65          70          75          80

Ile Glu Leu His Ala Lys Trp Gly Asn Arg Trp Ser Lys Ile Ala Lys
      85          90          95

His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Phe Trp Arg Thr
      100          105          110

Arg Ile Gln Lys His Ile Lys Gln Ala Glu Thr Ser Gln Gln His Gly
      115          120          125

Asn Ser Ser Glu Asn Ser Asn Asn Asp His Gln Ala Ser Asn Ser Thr
      130          135          140

Ser Lys Val Ser Thr Met Ala His Pro Asn Glu Thr Phe Ser Ser Pro
      145          150          155          160

Ser Tyr Gln Ala Thr Phe Glu Pro Phe Gln Pro Gln Phe Leu Gln Ser
      165          170          175

Met Ile Asn Gln Val Val Val Pro Ala Thr Thr Thr Ile Gly Ala Ser
      180          185          190

Arg Ile Ser Gly Arg Leu Cys Asn Tyr Ser Met Glu Ile Asn
      195          200          205

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```

<210> 35
<211> 863
<212> DNA
<213> Glycine max

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<400> 35
gcacgagctc tatcacacac acaagtcaat ggataaaaaa caacagtgta agacgtctca 60
agatcctgaa gtgagaaaaag ggccttggac aatggaagaa gacttgatct tgatgaacta 120
tattgcaaat catggggaag gtgtttggaa ctctttggcc aaagctgctg gtctcaaacg 180
taacggaaaag agttgccggc taaggtggct aaattacctc cgtcctgatg ttagaagagg 240
gaatattaca cccgaggaac aacttttgat tatggagctc cacgcaaagt ggggaaacag 300
gtggtcctaaa attgccaagc atctacctgg aaggactgat aatgagatca agaactattg 360
gaggacaagg atccagaagc acatcaagca agctgagaac tttcagcaac agagtagtaa 420
taattctgag ataaatgatc accaagctag cactagccat gtttccacca tggctgagcc 480
catggagatg tattctccac cctgttatca aggaatgtta gagccatttt caactcagtt 540
ccctacaatt aatcctgatc aatccagttg ttgtaccaat gacaacaaca acattaacta 600
ttggagcatg gaggatagct ggtcaatgca attactgaac ggtgattaaa tattatcaag 660
ataaaaccta agttytgaag ttccataagg ctggaatgtc tytggattaa aacatattat 720
tggttttgtt tatataagta gttggatgtt tggttttgcg taccattatt agctatgtgc 780
tgtaatatat acgagatytt atattaaact atatctgcat gctttatata taaaaaaaaa 840
aaaaaaaaaa aaaaaaaaaa aaa 863

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```

<210> 36
<211> 206
<212> PRT
<213> Glycine max

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<400> 36
Met Asp Lys Lys Gln Gln Cys Lys Thr Ser Gln Asp Pro Glu Val Arg
 1          5          10          15

Lys Gly Pro Trp Thr Met Glu Glu Asp Leu Ile Leu Met Asn Tyr Ile
          20          25          30

Ala Asn His Gly Glu Gly Val Trp Asn Ser Leu Ala Lys Ala Ala Gly
          35          40          45

Leu Lys Arg Asn Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu
          50          55          60

Arg Pro Asp Val Arg Arg Gly Asn Ile Thr Pro Glu Glu Gln Leu Leu
          65          70          75          80

Ile Met Glu Leu His Ala Lys Trp Gly Asn Arg Trp Ser Lys Ile Ala
          85          90          95

Lys His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Arg
          100          105          110

Thr Arg Ile Gln Lys His Ile Lys Gln Ala Glu Asn Phe Gln Gln Gln
          115          120          125

Ser Ser Asn Asn Ser Glu Ile Asn Asp His Gln Ala Ser Thr Ser His
          130          135          140

Val Ser Thr Met Ala Glu Pro Met Glu Met Tyr Ser Pro Pro Cys Tyr
          145          150          155          160

Gln Gly Met Leu Glu Pro Phe Ser Thr Gln Phe Pro Thr Ile Asn Pro
          165          170          175

Asp Gln Ser Ser Cys Cys Thr Asn Asp Asn Asn Asn Ile Asn Tyr Trp
          180          185          190

```

Ser Met Glu Asp Ser Trp Ser Met Gln Leu Leu Asn Gly Asp  
 195 200 205

<210> 37  
 <211> 805  
 <212> DNA  
 <213> Glycine max

<400> 37  
 aaaaaaacat gcaactcatc atctcatgat cctgaagtga gaaagggacc atggaccatg 60  
 gaagaagact tgatcttgat aaactatatt gcaaatacac gtgaagggtg ttggaactcc 120  
 ttagccaaag cttctggtct caaacgaacg ggaaagagtt gtcgactccg ttggctaaac 180  
 taccttcgtc ctgatgttag aagaggaaac attacaccg aggaacagct ttgatcata 240  
 gaacttcatg caaagtgggg caatagggtg tccaaaattg caaagcatct tccaggaaga 300  
 actgacaatg agattaagaa cttctggaga acaaggatcc aaaagcacat taagcaagct 360  
 gagacttcac aacaacatgg taattcagag aataatgatc atcaagcaag cactagtact 420  
 agcaaagtgt ccaccatggc acatccaaat gagactttct ctccaccctc ataccaagga 480  
 acttttgagc cattccaacc tcaattccct acaatcactg atcaatcaag ttgttgatcc 540  
 accaccaacg acaacaacaa ctattggagc atcgaggata tctggctcgtc tatgcaatta 600  
 ctcaatggag attaaaccta gctatatgca tgctatatata aatcatatat atgatgatat 660  
 ataaacctaa gctctttag agtgtgttca ggcttaataa catcattagg tctgtttata 720  
 tgagtgtct aagtttggtg tttgtaatgc atgatgtgag ttaagaatta atttagttat 780  
 ggttggaata aaaaaaaaaa aaaaa 805

<210> 38  
 <211> 204  
 <212> PRT  
 <213> Glycine max

<400> 38  
 Lys Lys Pro Cys Asn Ser Ser Ser His Asp Pro Glu Val Arg Lys Gly  
 1 5 10 15  
 Pro Trp Thr Met Glu Glu Asp Leu Ile Leu Ile Asn Tyr Ile Ala Asn  
 20 25 30  
 His Gly Glu Gly Val Trp Asn Ser Leu Ala Lys Ala Ser Gly Leu Lys  
 35 40 45  
 Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg Pro  
 50 55 60  
 Asp Val Arg Arg Gly Asn Ile Thr Pro Glu Glu Gln Leu Leu Ile Ile  
 65 70 75 80  
 Glu Leu His Ala Lys Trp Gly Asn Arg Trp Ser Lys Ile Ala Lys His  
 85 90 95  
 Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Phe Trp Arg Thr Arg  
 100 105 110  
 Ile Gln Lys His Ile Lys Gln Ala Glu Thr Ser Gln Gln His Gly Asn  
 115 120 125  
 Ser Glu Asn Asn Asp His Gln Ala Ser Thr Ser Thr Ser Lys Val Ser  
 130 135 140  
 Thr Met Ala His Pro Asn Glu Thr Phe Ser Pro Pro Ser Tyr Gln Gly  
 145 150 155 160

Thr Phe Glu Pro Phe Gln Pro Gln Phe Pro Thr Ile Thr Asp Gln Ser  
165 170 175

Ser Cys Cys Thr Thr Thr Asn Asp Asn Asn Asn Tyr Trp Ser Ile Glu  
180 185 190

Asp Ile Trp Ser Ser Met Gln Leu Leu Asn Gly Asp  
195 200

<210> 39  
<211> 751  
<212> DNA  
<213> Glycine max

<400> 39  
tggatgttaa gaaaggtggg tctgtagtac aagcacaagt gaagttgcag aagcataacg 60  
aaaaggagat gggcatgaga aaaggtccat gggcgggtga ggaggacacc attctggtca 120  
attacatcgc cacacacggt gaaggccact ggaattccgt ggcacgatgt gcaggtctaa 180  
ggaggagtgg gaagagttgc agattaaggt ggctaaacta cttgcgcccc gacgtgcggc 240  
gtggaaaatat cacactccaa gaacaaatat taattctcga ccttcactct cgctggggca 300  
acaggtggtc aaagattgct caacagctgc caggaagaac agacaacgaa ataaagaact 360  
attggaggac cagagtgata aaacaagcga agcagctaaa gtgcgatgtg aatagcaaac 420  
agttcagaga cacgttgctg tacgtttgga tgccgcgctt gctggagcgg cttcagcccc 480  
catcacaagc actggagcca aaccaaagtg gacttgtgtt acacgcttca tcatcactgc 540  
ttccttcgaa ttccgaccat agtattgaaa gggggtcgga tctgtggcca ggtttcaata 600  
accaaagtgt gttggaacag gggagtggcg gtgacttgtt ggaaagtgtg tgggatgacg 660  
acaatatgtg ctttttgcaa cagctttctt atgacctcca aatgaaataa aatacaattc 720  
ccttcctgca cgcaaaaaaa aaaaaaaaaa a 751

<210> 40  
<211> 235  
<212> PRT  
<213> Glycine max

<400> 40  
Asp Val Lys Lys Gly Gly Ser Val Val Gln Ala Gln Val Lys Leu Gln  
1 5 10 15

Lys His Asn Glu Lys Glu Met Gly Met Arg Lys Gly Pro Trp Ala Val  
20 25 30

Glu Glu Asp Thr Ile Leu Val Asn Tyr Ile Ala Thr His Gly Glu Gly  
35 40 45

His Trp Asn Ser Val Ala Arg Cys Ala Gly Leu Arg Arg Ser Gly Lys  
50 55 60

Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg Pro Asp Val Arg Arg  
65 70 75 80

Gly Asn Ile Thr Leu Gln Glu Gln Ile Leu Ile Leu Asp Leu His Ser  
85 90 95

Arg Trp Gly Asn Arg Trp Ser Lys Ile Ala Gln Gln Leu Pro Gly Arg  
100 105 110

Thr Asp Asn Glu Ile Lys Asn Tyr Trp Arg Thr Arg Val Ile Lys Gln  
115 120 125

Ala Lys Gln Leu Lys Cys Asp Val Asn Ser Lys Gln Phe Arg Asp Thr  
130 135 140

Leu Arg Tyr Val Trp Met Pro Arg Leu Leu Glu Arg Leu Gln Pro Thr  
145 150 155 160

Ser Gln Ala Leu Glu Pro Asn Gln Ser Gly Leu Val Leu His Ala Ser  
165 170 175

Ser Ser Leu Leu Pro Ser Asn Ser Asp His Ser Ile Glu Arg Gly Ser  
180 185 190

Asp Leu Trp Pro Gly Phe Asn Asn Gln Met Leu Leu Glu Gln Gly Ser  
195 200 205

Gly Gly Asp Leu Leu Glu Ser Leu Trp Asp Asp Asp Asn Met Cys Phe  
210 215 220

Leu Gln Gln Leu Ser Tyr Asp Leu Gln Met Lys  
225 230 235

<210> 41  
<211> 500  
<212> DNA  
<213> Glycine max

<400> 41  
catttctaatt tgttctgata catatatatc atactttctt tgtaataact taaagaaccc 60  
cacaaaaaca ccaaccatgt ccacaattgc aaagagagat ttgagttcta atgaagaaga 120  
gagtgagctg agaagaggtc cttggactct tgaagaagac agcttactca tacactatat 180  
tgctcgtcat ggtgaaggcc gttggaatat gttagccaaa agtgcaggat tgaagaggac 240  
tgaaaaaagt tgcagactta gatggctgaa ttatttgaaa ccagacatta agagagggaa 300  
cctcactcca caggagcaac tcttgatcct tgaactccat tccaagtggg gtaacagggtg 360  
gtcaaaaatt gctcagcatc tgccaggaag aacagacaat gagatcaaga actattggag 420  
aacaaggata cagaaacagg gcacgccaac ttaacattga atctggtagc aagagattca 480  
ttgatgctgt cagtgttttt 500

<210> 42  
<211> 229  
<212> PRT  
<213> Glycine max

<220>  
<221> UNSURE  
<222> (138)

<400> 42  
Met Ser Thr Ile Ala Lys Arg Asp Leu Ser Ser Asn Glu Glu Glu Ser  
1 5 10 15

Glu Leu Arg Arg Gly Pro Trp Thr Leu Glu Glu Asp Ser Leu Leu Ile  
20 25 30

His Tyr Ile Ala Arg His Gly Glu Gly Arg Trp Asn Met Leu Ala Lys  
35 40 45

Ser Ala Gly Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu  
50 55 60

Asn Tyr Leu Lys Pro Asp Ile Lys Arg Gly Asn Leu Thr Pro Gln Glu  
 65 70 75 80  
 Gln Leu Leu Ile Leu Glu Leu His Ser Lys Trp Gly Asn Arg Trp Ser  
 85 90 95  
 Lys Ile Ala Gln His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn  
 100 105 110  
 Tyr Trp Arg Thr Arg Ile Gln Lys Gln Ala Arg Gln Leu Asn Ile Glu  
 115 120 125  
 Ser Gly Ser Lys Arg Phe Ile Asp Ala Xaa Lys Cys Phe Trp Met Pro  
 130 135 140  
 Arg Leu Leu Gln Lys Met Glu Gln Ser Asn Ser Pro Ser Pro His His  
 145 150 155 160  
 Ser Ser Met Thr Asn Met Met Asn Leu Gly Asn Ser Gly Glu Ala Ser  
 165 170 175  
 Met Ser Ser Met Ser Ser Ser Phe Asn Ile Asn Pro Ser Met Ser Ser  
 180 185 190  
 Ser Ser Ser Pro Pro Lys Gly Asn Leu Leu Trp Met Met Pro Asn His  
 195 200 205  
 Phe Lys Tyr Tyr Val Gln Pro His Gln Ser Ile Pro Arg Phe Leu Pro  
 210 215 220  
 Ile Phe Thr Ala Thr  
 225

<210> 43  
 <211> 1348  
 <212> DNA  
 <213> Glycine max

<400> 43  
 tacctctcca accaagacca atttgaaaac ctcttcaatc caacaaacaa acgttctccc 60  
 ttttgttctg agagaatcaa tggatggaaa aggagcaaga agtagcaaca cccttttaag 120  
 tagtgaggac gagatggacc ttcgaagagg cccttggacc gtcgatgaag acctcactct 180  
 tatcaattac gttgccactc atggcggaagg tcgctggaat accctcgccc tctctgctgg 240  
 gctgaaacga acgggggaaga gttgcagatt gaggtggctg aattatctgc gtcctgatgt 300  
 tcgacgtgga aacatcacgc ttgaagaaca acttttgatt ctggagctcc attctcgctg 360  
 gggaaaccga tggtcgaaaa ttgctcaata tttgcctggg agaaccgaca atgagataaa 420  
 gaactatttg agaaccctgt tccaaaagca tgccaagcaa ctcaaatgcg acgtgaatag 480  
 caagcaattc aaggacacca tgcgttatcat ttgatgcca aggctcgtgg aacgcattca 540  
 agccaccgct gccgcctccg caccacaacc cgttaccgta ccaccgcgac caacaatgca 600  
 tacacctacg gaagcaacct taataacaac aaattcgagg ttcacgatca caagggcaaa 660  
 atgggggttaa ccgatccttc agttatgaac aatgacttaa tgggttcaca tgtcacgcaa 720  
 agttacaccc ctgagaatag tagcaccggt gcgctcatcat cagactcgtt tgggactcaa 780  
 gtctcagcaa tttctgattt gactgaatat tacactgtca ctggtagtgg taacaataac 840  
 aatactaatt ctgocgatta ttatcaaccc tctcaaatta gttactcgga tagttgcattc 900  
 acaagcccat ctgggttggt ccoctcaaggg ctagattttc aatccatgga tccaaacacc 960  
 ccgtggaaca tgcaaaagtgg ggactcctct gacagttttt ggaacgttga aagcatgttg 1020  
 ttcttagagc agcaactcat gaatgacaac atgtgaaaac attgggaata ggaaaataag 1080  
 acctagatac ggttcttctt agtatttgtt ttttaattaaa gttaaagtta acacaagtta 1140  
 ttgaagtgaac actttaattt taattgaata ataatactga aaacaagagt tgtattttaag 1200  
 ttttattctt ttatgaatta tgaattagat tgacagaagg gggtgtttgt gaaatatata 1260

ggtgaaagta tagaaagtag caacattaat aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1320  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1348

<210> 44  
 <211> 196  
 <212> PRT  
 <213> Glycine max

<400> 44  
 Met Asp Gly Lys Gly Ala Arg Ser Ser Asn Thr Leu Leu Ser Ser Glu  
 1 5 10 15  
 Asp Glu Met Asp Leu Arg Arg Gly Pro Trp Thr Val Asp Glu Asp Leu  
 20 25 30  
 Thr Leu Ile Asn Tyr Val Ala Thr His Gly Glu Gly Arg Trp Asn Thr  
 35 40 45  
 Leu Ala Leu Ser Ala Gly Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu  
 50 55 60  
 Arg Trp Leu Asn Tyr Leu Arg Pro Asp Val Arg Arg Gly Asn Ile Thr  
 65 70 75 80  
 Leu Glu Glu Gln Leu Leu Ile Leu Glu Leu His Ser Arg Trp Gly Asn  
 85 90 95  
 Arg Trp Ser Lys Ile Ala Gln Tyr Leu Pro Gly Arg Thr Asp Asn Glu  
 100 105 110  
 Ile Lys Asn Tyr Trp Arg Thr Arg Val Gln Lys His Ala Lys Gln Leu  
 115 120 125  
 Lys Cys Asp Val Asn Ser Lys Gln Phe Lys Asp Thr Met Arg Tyr Ile  
 130 135 140  
 Trp Met Pro Arg Leu Val Glu Arg Ile Gln Ala Thr Ala Ala Ala Ser  
 145 150 155 160  
 Ala Pro Gln Pro Val Thr Val Pro Pro Arg Pro Thr Met His Thr Pro  
 165 170 175  
 Thr Glu Ala Thr Leu Ile Thr Thr Asn Ser Arg Phe Thr Ile Thr Arg  
 180 185 190  
 Ala Lys Trp Gly  
 195

<210> 45  
 <211> 1236  
 <212> DNA  
 <213> Glycine max

<220>  
 <221> unsure  
 <222> (519)

<220>  
 <221> unsure  
 <222> (521)

<220>  
 <221> unsure  
 <222> (530)..(531)

<220>  
 <221> unsure  
 <222> (534)

<220>  
 <221> unsure  
 <222> (800)

<220>  
 <221> unsure  
 <222> (1124)

<220>  
 <221> unsure  
 <222> (1151)

<400> 45  
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 aaacttaatt tcttttgttt tgagtttctt agagaatgga tgaaaaagga gcaagaagta 120  
 gcaacaccct tttaagttgt gaggacgaga tggaccttcg aagaggccct tggaccgtcg 180  
 atgaagacct cactcttatc aattacattg ccactcatgg cgaagggtcg tggaaacacgc 240  
 tcgcccctctc tgctgggctg aaacgaacgg ggaagagttg cagattgagg tggctgaatt 300  
 atctgcgtcc tgatgttcga cgtggaaaca tcacacttga agaacaactt ttgattctgg 360  
 agcttcattc tcgctgggga aaccgttggg cgaaaattgc tcaatatttg cctggtagaa 420  
 ccgacaacga gataaagaac tattggagaa cccgtgtcca aaagcatgcc aagcaactca 480  
 aatgtgacgt gaatagcaag caattcaagg acaccatgng ntacctttgn natnccaagg 540  
 ctgctggaac gcattcaagc agcggcgacg gcccccgtaa ccaccaccgt aactgcgggc 600  
 gccaccaaca atgcattcac ctacgggraac aaccttatac caccaaattc gaggttctga 660  
 atcacaaggg cagaatgggg ttaaccgatc cttcagttgc gaacaatgac ttigtgggtt 720  
 cacatgtcac gcaaaggtag cctactcctg agaatagtag cacgggtgcg tcatcatcag 780  
 actcgtttgg gactcaagtn tcaacaattt ctgatttgac tgaaaattcc agtgtccctg 840  
 aaaatactaa ttctgcggat tattatcaac cctctcaaat tagtaattac tcggataatt 900  
 gcatcacaag cccatctggg ttcttggtcc ctcaaggact agatcttcaa tccatggatc 960  
 caaacacacc gtggaacatg caaagtgggg actcctctga caattttttg gacgttgaaa 1020  
 gcatgttatt cttagagcag caactcatga atgacaacat gtgaaacatt ggggaatagga 1080  
 aaataagact tagatacggg tcttctaata ttttttagtg ktgngtttta attaaagtta 1140  
 aagttaacac nagttattga agtgaaactt taattttaat taaataataa tcctgaaaaa 1200  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 1236

<210> 46  
 <211> 322  
 <212> PRT  
 <213> Glycine max

<220>  
 <221> UNSURE  
 <222> (142)

<220>  
 <221> UNSURE  
 <222> (145)..(146)..(147)

<220>  
 <221> UNSURE  
 <222> (178)



<400> 46

Met Asp Glu Lys Gly Ala Arg Ser Ser Asn Thr Leu Leu Ser Cys Glu  
1 5 10 15

Asp Glu Met Asp Leu Arg Arg Gly Pro Trp Thr Val Asp Glu Asp Leu  
20 25 30

Thr Leu Ile Asn Tyr Ile Ala Thr His Gly Glu Gly Arg Trp Asn Thr  
35 40 45

Leu Ala Leu Ser Ala Gly Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu  
50 55 60

Arg Trp Leu Asn Tyr Leu Arg Pro Asp Val Arg Arg Gly Asn Ile Thr  
65 70 75 80

Leu Glu Glu Gln Leu Leu Ile Leu Glu Leu His Ser Arg Trp Gly Asn  
85 90 95

Arg Trp Ser Lys Ile Ala Gln Tyr Leu Pro Gly Arg Thr Asp Asn Glu  
100 105 110

Ile Lys Asn Tyr Trp Arg Thr Arg Val Gln Lys His Ala Lys Gln Leu  
115 120 125

Lys Cys Asp Val Asn Ser Lys Gln Phe Lys Asp Thr Met Xaa Tyr Leu  
130 135 140

Xaa Xaa Xaa Lys Ala Arg Gly Thr His Ser Ser Ser Gly Asp Gly Pro  
145 150 155 160

Arg Asn His His Arg Asn Cys Gly Arg His Gln Gln Cys Ile His Leu  
165 170 175

Arg Xaa Gln Pro Tyr Thr Thr Lys Phe Glu Val Leu Asn His Lys Gly  
180 185 190

Arg Met Gly Leu Thr Asp Pro Ser Val Ala Asn Asn Asp Phe Val Gly  
195 200 205

Ser His Val Thr Gln Arg Tyr Pro Thr Pro Glu Asn Ser Ser Thr Gly  
210 215 220

Ala Ser Ser Ser Asp Ser Phe Gly Thr Gln Val Ser Thr Ile Ser Asp  
225 230 235 240

Leu Thr Glu Asn Ser Ser Val Pro Glu Asn Thr Asn Ser Ala Asp Tyr  
245 250 255

Tyr Gln Pro Ser Gln Ile Ser Asn Tyr Ser Asp Asn Cys Ile Thr Ser  
260 265 270

Pro Ser Gly Phe Leu Phe Pro Gln Gly Leu Asp Leu Gln Ser Met Asp  
275 280 285

Pro Asn Thr Pro Trp Asn Met Gln Ser Gly Asp Ser Ser Asp Asn Phe  
290 295 300

Trp Asp Val Glu Ser Met Leu Phe Leu Glu Gln Gln Leu Met Asn Asp  
 305 310 315 320

Asn Met

<210> 47  
 <211> 1181  
 <212> DNA  
 <213> Glycine max

<400> 47  
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 gacaatgaac ttagaagagg gccttggact ctggaagagg ataacttgct ctcccaatat 120  
 atttttaatc atggggaagg gcgatggaat ttgctggcta aacgttcagg attaaagaga 180  
 actgggaaaaa gttgcagatt aaggtggcta aattatctaa agccagatgt aaaacgggga 240  
 aatttaaccc cacaagagca acttataatt ctggaactcc actcaaagtg gggaaacagg 300  
 tgggtcaaaaa ttgcacaaca tttgccaggc agaacagaca atgaaatcaa gaactattgg 360  
 agaactagga ttcagaaaca agcaagacat ttgaaaattht acactgacag cagagagtht 420  
 caagaacttg ttaggcgttt ctggatgcct agattgcttc agaaagcaaa agaathcatc 480  
 tcttcaaaaa tgtcaattca aaaccaggca attcctatgc cttttgatta tgtttctcag 540  
 catttaactg ttgggaccat acctccttgg cagggacctt gtatgaatga agctgggtccc 600  
 acttacatgg accaathcatga gcagactcag actcggaaca ccaathcatg ttcathcatc 660  
 tccttgtctg agtcagcaaa tathcaaaaa gtgcctcagc attttggaca caccaccatc 720  
 acccaatttc atgccttgaa taccaatgac tttggcacct tcacathatga aggttataat 780  
 gtaacaaca atgtctatga gatggacaac ttcaaaacga ctactacatg ggtggctgag 840  
 gatgcgcaat acccaattgg tgattgtcaa atggtaggaa gcaattgggt aaacaacgat 900  
 tttgcathga acathgtgaa catggatgaa ctgtggcagt ttagcaagtt aaaaaataa 960  
 gattttagggt ttttgttttt tttggaataa ccaaaagtc ccaactcttt ctttgatgac 1020  
 gttattattg ttathcatgaa ctgtggatta gctaccgaat taattaatac agatggcgat 1080  
 tgttttctgt acathctgtct tgtattactc tgttcagata agtacttttg taatttgtat 1140  
 tgattgagaa aagtcathaa ttagtcacta gtacaaaaaa a 1181

<210> 48  
 <211> 312  
 <212> PRT  
 <213> Glycine max

<400> 48  
 Met Ser Thr Ser Lys Ser Val Ser Ser Ser Ser Glu Asp Asp Asn Glu  
 1 5 10 15  
 Leu Arg Arg Gly Pro Trp Thr Leu Glu Glu Asp Asn Leu Leu Ser Gln  
 20 25 30  
 Tyr Ile Phe Asn His Gly Glu Gly Arg Trp Asn Leu Leu Ala Lys Arg  
 35 40 45  
 Ser Gly Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn  
 50 55 60  
 Tyr Leu Lys Pro Asp Val Lys Arg Gly Asn Leu Thr Pro Gln Glu Gln  
 65 70 75 80  
 Leu Ile Ile Leu Glu Leu His Ser Lys Trp Gly Asn Arg Trp Ser Lys  
 85 90 95  
 Ile Ala Gln His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr  
 100 105 110

Trp Arg Thr Arg Ile Gln Lys Gln Ala Arg His Leu Lys Ile Tyr Thr  
 115 120 125  
 Asp Ser Arg Glu Phe Gln Glu Leu Val Arg Arg Phe Trp Met Pro Arg  
 130 135 140  
 Leu Leu Gln Lys Ala Lys Glu Ser Ser Ser Asn Met Ser Ile Gln  
 145 150 155 160  
 Asn Gln Ala Ile Pro Met Pro Phe Asp Tyr Val Ser Gln His Leu Thr  
 165 170 175  
 Val Gly Thr Ile Pro Pro Trp Gln Gly Pro Cys Met Asn Glu Ala Gly  
 180 185 190  
 Pro Thr Tyr Met Asp Gln His Glu Gln Thr Gln Thr Arg Asn Thr Asn  
 195 200 205  
 Asn Gly Ser Cys Ile Ser Leu Ser Glu Ser Ala Asn Ile Pro Lys Val  
 210 215 220  
 Pro Gln His Phe Gly His Thr Thr Ile Thr Gln Phe His Ala Leu Asn  
 225 230 235 240  
 Thr Asn Asp Phe Gly Thr Phe Thr Tyr Glu Gly Tyr Asn Val Asn Asn  
 245 250 255  
 Asn Val Tyr Glu Met Asp Asn Phe Lys Thr Thr Thr Thr Trp Val Ala  
 260 265 270  
 Glu Asp Ala Gln Tyr Pro Ile Gly Asp Cys Gln Met Val Gly Ser Asn  
 275 280 285  
 Trp Val Asn Asn Asp Phe Ala Cys Asn Met Trp Asn Met Asp Glu Leu  
 290 295 300  
 Trp Gln Phe Ser Lys Leu Gln Lys  
 305 310

<210> 49  
 <211> 1186  
 <212> DNA  
 <213> Glycine max

<400> 49  
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 tagtcatgga gaagggcgat ggaatttgct agctaaacgt tcaggattaa agcgaactgg 180  
 gaaaagtgtc agattaaggt ggctaaatta tctaaagcca gatgtaaaac ggggaaattt 240  
 aacccacaaa gagcaactta taatcctcga actocactca aagtggggaa acaggtggtc 300  
 aaaaattgca caaaatttgc caggcagaac agacaatgaa atcaagaact attggagaac 360  
 taggattcag aaacaagcaa gacatttgaa aattgacact gacaccagag agtttcagga 420  
 acttggttagg cgtttctgga tgccatagatg cttcaaaaag cccaagaatc atcttcttca 480  
 gccatgtcaa ttcaaaacca ggcaactcct atgccttttg atggtgtttc tcagcattca 540  
 actgtttgga ccataccatc acattcacac accccttggc agggaccttg tatgaatgaa 600  
 gctggtccca cttacatgga ccaacatgag cagaactcag actctgaaca caacaatggt 660  
 tcatgcatct ccttgctcga gtcagcaaat ttccaaaag tgccctcagca ttttgacgc 720  
 accaccatca cccaatatca tgccctgaat aacaatgact ttggcacctt cacatatgac 780  
 ggctacaatg taagcaacaa tgtctatgag atggacaact tcaaaacgcc tactacaagg 840  
 gtggctgagg atgcgcaata cccaactggt gattgtcaaa tggttaggaag caattgggta 900

aacagcgatt ttgcatgtaa catgtggaac atggatgaat tgtggcaatt tagcaagtta 960  
caaaaaataag atttttaggt ttgggttttt ttggagttacc aagactctat ctttggtgat 1020  
gttattattg ttatcatgaa ctgttgatta gctactacca aattaattaa tacagatggg 1080  
gattgttttc tgtacatctg ttttgcatta ctctgttttg caatttgat tgattgagaa 1140  
aagtcattaa ttagtcacta gttcaaaaca caaaaaaaaa aaaaaa 1186

<210> 50  
<211> 192  
<212> PRT  
<213> Glycine max

<400> 50  
Met Ser Thr Ser Lys Ser Val Ser Ser Ser Ser Glu Asp Asp Asn Glu  
1 5 10 15  
Leu Arg Arg Gly Pro Trp Thr Leu Glu Glu Asp Asn Leu Leu Ser Gln  
20 25 30  
Tyr Ile Ser Ser His Gly Glu Gly Arg Trp Asn Leu Leu Ala Lys Arg  
35 40 45  
Ser Gly Leu Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn  
50 55 60  
Tyr Leu Lys Pro Asp Val Lys Arg Gly Asn Leu Thr Pro Gln Glu Gln  
65 70 75 80  
Leu Ile Ile Leu Glu Leu His Ser Lys Trp Gly Asn Arg Trp Ser Lys  
85 90 95  
Ile Ala Gln Asn Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr  
100 105 110  
Trp Arg Thr Arg Ile Gln Lys Gln Ala Arg His Leu Lys Ile Asp Thr  
115 120 125  
Asp Thr Arg Glu Phe Gln Glu Leu Val Arg Arg Phe Trp Met Pro Arg  
130 135 140  
Cys Phe Lys Lys Pro Lys Asn His Leu Leu Gln Pro Cys Gln Phe Lys  
145 150 155 160  
Thr Arg Gln Leu Leu Cys Leu Leu Met Val Phe Leu Ser Ile Gln Leu  
165 170 175  
Leu Gly Pro Tyr His His Ile His Thr Pro Leu Gly Arg Asp Leu Val  
180 185 190

<210> 51  
<211> 487  
<212> DNA  
<213> Glycine max

<220>  
<221> unsure  
<222> (358)

<220>  
<221> unsure  
<222> (429)

<400> 51  
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agatagagag aggaaaacga cctatatattt ttttcotttg agagcttcag gggctaggaa 120  
aattagaagg acagccacaa gtataaaggc ggtgaaataa aagagaaaga caagaaggag 180  
acatgggaag accaccttgt tgtgacaaag aaggggtcaa gaaagggcct tggactcctg 240  
aagaagacat catattgggtg tcttatattc aggaacatgg tcctggaaat tggagggcag 300  
ttcctgccaa aacaggggtg tcaagatgca gcaagagttg cagacttaga tggacgantt 360  
acctgaggcc aggaatcaag cgtggtaact tcacaagaac aagaggagaa gatgataatc 420  
catcttcang atcttttagg aaacagatgg ggtgcaatag cttcatacct tcacaaaagg 480  
acaaggg 487

<210> 52  
<211> 90  
<212> PRT  
<213> Glycine max

<220>  
<221> UNSURE  
<222> (59)

<220>  
<221> UNSURE  
<222> (72)

<220>  
<221> UNSURE  
<222> (83)

<400> 52  
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1 5 10 15  
Trp Thr Pro Glu Glu Asp Ile Ile Leu Val Ser Tyr Ile Gln Glu His  
20 25 30  
Gly Pro Gly Asn Trp Arg Ala Val Pro Ala Lys Thr Gly Leu Ser Arg  
35 40 45  
Cys Ser Lys Ser Cys Arg Leu Arg Trp Thr Xaa Tyr Leu Arg Pro Gly  
50 55 60  
Ile Lys Arg Gly Asn Phe Thr Xaa Glu Gln Glu Glu Lys Met Ile Ile  
65 70 75 80  
His Leu Xaa Asp Leu Leu Gly Asn Arg Trp  
85 90

<210> 53  
<211> 1556  
<212> DNA  
<213> Glycine max

<400> 53  
gcacgaggag aaataaaaaag agaagaaaga aaacacgata gtatcatcat atcaccacca 60  
cacacataga tagagagagg aaaacgacct atattttttt tcctttgaga gcttcagggg 120  
ctaggaaaaat tagaaggaca gccacaagta taaaggcggg gaaataaaaag agaaagacaa 180  
gaaggagaca tgggaagacc accttggtgt gacaaagaag gggtaagaa agggccttgg 240  
actcctgaag aagacatcat attggtgtct tatattcagg aacatgggtcc tggaaattgg 300  
agggcagttc ctgccaaaac agggttgtca agatgcagca agagttgcag acttagatgg 360

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acgaattacc tgaggccagg aatcaagcgt ggtaacttca cagaacaaga ggagaagatg 420
ataatccatc ttcaagatct tttaggaaac agatgggctg caatagcttc ataccttcca 480
caaagaacag acaatgacat aaagaactat tggaataccc atttgagaaa gaagctgaag 540
aagatgcaag caggcggtag aggtggtagc tttggagaag ggttttcagc ctcaaggcaa 600
atccctagag gccagtggga aagaaggctc caaactgata tccaaatggc aaagagagcc 660
ctcagtgaag ctctttcacc agagaaaaag ccatcttggt tatctgcctc aaactcaaac 720
ccttcagata gtagcagctc cttctcttcc acaaaaccaa caacaacaca atctgtgtgc 780
tatgcatcaa gtgctgacaa catagctaga atgctcaagg gttggatgaa gaaccacca 840
aagtcctcaa gaaccaactc gtctatgact cagaactcat tcaacaactt agcagggtgct 900
gatactgctt gtagtagtgg agcaaaggga ccactaagca gtgccgaatt gtctgagaat 960
aattttgaat ccttgtttga ttttgatcag tctttggagt cttcaaactc tgatcaattc 1020
tctcagtcct tgtctcctga ggccactggt ttgcaagatg aaagcaagcc tgatattaat 1080
attgctgcag aaattatgcc cttctctttg cttgagaaat ggctccttga tgaggcaggt 1140
tgccaagaga aattagttgg ttggttggtg gatgccaaat ttttctaagt tgggttcatt 1200
ttgtgacata tgagactgtg ggattttttt attttatttt attttatttc ataagttata 1260
ggtagggcct catcaattaa tctcgcttcg gccttattag agagagaagt tttccagcct 1320
ttggtgctag acgtgtatat gttaattatt attgacatta tgatgattat tatcatactg 1380
tgtagttgc catacactgg caaacttgct tctcttatgt aaagttgatc ttgcgacgag 1440
atcctgcttt atggctttag gcagcgcgac cggctcttct tctttgtgtc gcttgattag 1500
taaccccccc cggggggggc cggggtccaa atccccctta atgggggtcct ttttag 1556

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<210> 54
<211> 332
<212> PRT
<213> Glycine max

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<400> 54
Met Gly Arg Pro Pro Cys Cys Asp Lys Glu Gly Val Lys Lys Gly Pro
 1             5             10             15

Trp Thr Pro Glu Glu Asp Ile Ile Leu Val Ser Tyr Ile Gln Glu His
          20             25             30

Gly Pro Gly Asn Trp Arg Ala Val Pro Ala Lys Thr Gly Leu Ser Arg
          35             40             45

Cys Ser Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Gly
          50             55             60

Ile Lys Arg Gly Asn Phe Thr Glu Gln Glu Glu Lys Met Ile Ile His
          65             70             75             80

Leu Gln Asp Leu Leu Gly Asn Arg Trp Ala Ala Ile Ala Ser Tyr Leu
          85             90             95

Pro Gln Arg Thr Asp Asn Asp Ile Lys Asn Tyr Trp Asn Thr His Leu
          100            105            110

Arg Lys Lys Leu Lys Lys Met Gln Ala Gly Gly Glu Gly Gly Ser Phe
          115            120            125

Gly Glu Gly Phe Ser Ala Ser Arg Gln Ile Pro Arg Gly Gln Trp Glu
          130            135            140

Arg Arg Leu Gln Thr Asp Ile Gln Met Ala Lys Arg Ala Leu Ser Glu
          145            150            155            160

Ala Leu Ser Pro Glu Lys Lys Pro Ser Cys Leu Ser Ala Ser Asn Ser
          165            170            175

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Asn Pro Ser Asp Ser Ser Ser Ser Phe Ser Ser Thr Lys Pro Thr Thr  
 180 185 190  
 Thr Gln Ser Val Cys Tyr Ala Ser Ser Ala Asp Asn Ile Ala Arg Met  
 195 200 205  
 Leu Lys Gly Trp Met Lys Asn Pro Pro Lys Ser Ser Arg Thr Asn Ser  
 210 215 220  
 Ser Met Thr Gln Asn Ser Phe Asn Asn Leu Ala Gly Ala Asp Thr Ala  
 225 230 235 240  
 Cys Ser Ser Gly Ala Lys Gly Pro Leu Ser Ser Ala Glu Leu Ser Glu  
 245 250 255  
 Asn Asn Phe Glu Ser Leu Phe Asp Phe Asp Gln Ser Leu Glu Ser Ser  
 260 265 270  
 Asn Ser Asp Gln Phe Ser Gln Ser Leu Ser Pro Glu Ala Thr Val Leu  
 275 280 285  
 Gln Asp Glu Ser Lys Pro Asp Ile Asn Ile Ala Ala Glu Ile Met Pro  
 290 295 300  
 Phe Ser Leu Leu Glu Lys Trp Leu Leu Asp Glu Ala Gly Cys Gln Glu  
 305 310 315 320  
 Lys Leu Val Gly Cys Cys Gly Asp Ala Lys Phe Phe  
 325 330

<210> 55  
 <211> 357  
 <212> DNA  
 <213> Triticum aestivum

<220>  
 <221> unsure  
 <222> (259)

<220>  
 <221> unsure  
 <222> (307)

<220>  
 <221> unsure  
 <222> (319)

<400> 55  
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 tttgcgcaaa gtcgcaacaa caaatgtcac ctttgctaata aactttcttc ttgcttcaac 120  
 ctctgtaatc tccatgcagg cctcaaccgc acaggaaaga gctgtcgctt ccgggtgggtt 180  
 aactacctcc accctgggoc taaagcgtgg ggcgatgact ccccatgaaa gaacgcctca 240  
 tctccaact ccatgctong tggggaaaca agtgggtcaa ggataacacg gaactgcca 300  
 ggcgtancga caatgaatna aagaactact gggagaacac atttgaggaa aaggaag 357

<210> 56  
 <211> 54  
 <212> PRT  
 <213> Triticum aestivum

<220>  
 <221> UNSURE  
 <222> (21)

<220>  
 <221> UNSURE  
 <222> (27)..(28)

<220>  
 <221> UNSURE  
 <222> (41)

<400> 56  
 Ala Gly Leu Asn Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Val Asn  
 1 5 10 15

Tyr Leu His Pro Xaa Leu Lys Arg Gly Arg Xaa Xaa Pro Met Lys Glu  
 20 25 30

Arg Leu Ile Leu Gln Leu His Ala Xaa Trp Gly Asn Lys Trp Ser Lys  
 35 40 45

Asp Asn Thr Glu Leu Pro  
 50

<210> 57  
 <211> 1072  
 <212> DNA  
 <213> Triticum aestivum

<400> 57  
 gcacgaggcc aaagtatcag gtttgagggg tgggggatcc aaaaattagg tagctatatatt 60  
 gaagtatttt ggcgaaagtc gcaacaacaa atgtcacctt tgctaataac tttcttcttg 120  
 cttcaacctc tgtaatctcc atgcaggcct caaccgcaca ggaaagagct gtögcctccg 180  
 gtgggttaac tacctccacc ctggcctaaa gcgtgggögc atgactcccc atgaagaacg 240  
 cctcatcctc gagctccatg ctögggtgggg aaacagggtg tccaggatag cacggaagct 300  
 gccaggöcgt accgacaatg agatcaagaa ctactggaga acacatatga ggaagaaagc 360  
 acaggagagg aagaggagcg tgtcacccctc accatcttca tctcagtga cataccaatc 420  
 cattcagcca cagacgccat cgatcatggg aattggcöag caggaaacttc atögtggcag 480  
 tagctgcatc acaagcatat tgaaggöcac gcctgctgac atögatögat acctcatgga 540  
 tcagatatgg atöggagattg aggcacccctc tggögtcaac tttcatgacg ggaaggataa 600  
 ttcatacagc agccöctctg gccctctgct gccatcacöc atötgöggatt actacagccc 660  
 tgaggcaggc tggaagatgg atgagataaa gatöggccöc caagttagct acagtaaagg 720  
 aattöggccc agttattgaa gccatatata ttötatcaga ttactaagtt acttgcaacc 780  
 tagcagaagt gaaatgcttt töttgaaaga accattagca tggatctaaa aaatatttat 840  
 atctatctag cattccaagt gtöctcatgt tttatötatc tactatötag catctagtgt 900  
 gcaagacatg taatöcaagg acacttccac tttötatöca caataatcag ctatctcctg 960  
 taagactttt ccaatöcaaa catöattagc aggtötaata tcaactöaaa töcttgccaa 1020  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 1072

<210> 58  
 <211> 198  
 <212> PRT  
 <213> Triticum aestivum

<400> 58  
 Ala Gly Leu Asn Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Val Asn  
 1 5 10 15



Tyr Leu His Pro Gly Leu Lys Arg Gly Arg Met Thr Pro His Glu Glu  
                   20                                  25                                  30  
 Arg Leu Ile Leu Glu Leu His Ala Arg Trp Gly Asn Arg Trp Ser Arg  
                   35                                  40                                  45  
 Ile Ala Arg Lys Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr  
                   50                                  55                                  60  
 Trp Arg Thr His Met Arg Lys Lys Ala Gln Glu Arg Lys Arg Ser Val  
                   65                                  70                                  75                                  80  
 Ser Pro Ser Pro Ser Ser Ser Ser Val Thr Tyr Gln Ser Ile Gln Pro  
                                   85                                  90                                  95  
 Gln Thr Pro Ser Ile Met Gly Ile Gly Glu Gln Glu Leu His Gly Gly  
                                   100                                  105                                  110  
 Ser Ser Cys Ile Thr Ser Ile Leu Lys Gly Thr Pro Ala Asp Met Asp  
                   115                                  120                                  125  
 Gly Tyr Leu Met Asp Gln Ile Trp Met Glu Ile Glu Ala Pro Ser Gly  
                   130                                  135                                  140  
 Val Asn Phe His Asp Gly Lys Asp Asn Ser Tyr Ser Ser Pro Ser Gly  
                   145                                  150                                  155                                  160  
 Pro Leu Leu Pro Ser Pro Met Trp Asp Tyr Tyr Ser Pro Glu Ala Gly  
                                   165                                  170                                  175  
 Trp Lys Met Asp Glu Ile Lys Met Ala Pro Gln Val Ser Tyr Ser Lys  
                   180                                  185                                  190  
 Gly Ile Gly Pro Ser Tyr  
                   195

<210> 59  
 <211> 521  
 <212> DNA  
 <213> Triticum aestivum

<220>  
 <221> unsure  
 <222> (108)

<220>  
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<220>  
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<220>  
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<222> (434)

<220>  
<221> unsure  
<222> (447)

<220>  
<221> unsure  
<222> (456)

<220>  
<221> unsure  
<222> (459)

<400> 59  
cttggatcct ccactagcta cgtcgtccat ggatgtggtg ctgcagagtc gtagcagcaa 60  
cagcatggcg gcggagccgg aggaggaggc ggaccggagg aggaggcnng agctccggcg 120  
agggccgtgg acggtggacg aggaccttac gctgatcaac tacatcgcg accacggcga 180  
gggccgctgg aacgcgctgg cgcgggcccgc cggcctgagg cgcacgggga agagctgccg 240  
gctgcggtgg ctgaactacc tccgccccga cgtgaagcgc ggcaacttca ccgccgacga 300  
gcagctcctc atcctcgacc tccactctcg ctggggcaac cggtggtcga agatngcgca 360  
ncacctcccg ggtcggacgg acaacgaaga tnaaagaact actgggagga ccanggtgca 420  
aaaagcacgc naancaactc aactgcnaac tccggnannc gcaaccttta aaggatgcca 480  
ataagggtacc tctggatgcc tcgcctctca acgcatcaac c 521

<210> 60  
<211> 131  
<212> PRT  
<213> Triticum aestivum

<220>  
<221> UNSURE  
<222> (27)

<220>  
<221> UNSURE  
<222> (109)

<220>  
<221> UNSURE  
<222> (111)

<220>  
<221> UNSURE  
<222> (122)

<220>  
<221> UNSURE  
<222> (129)

<400> 60  
Met Asp Val Val Leu Gln Ser Arg Ser Ser Asn Ser Met Ala Ala Glu  
1 5 10 15

Pro Glu Glu Glu Ala Asp Arg Arg Arg Arg Xaa Glu Leu Arg Arg Gly  
20 25 30

Pro Trp Thr Val Asp Glu Asp Leu Thr Leu Ile Asn Tyr Ile Ala Asp  
35 40 45

His Gly Glu Gly Arg Trp Asn Ala Leu Ala Arg Ala Ala Gly Leu Arg  
50 55 60

Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg Pro  
65 70 75 80

Asp Val Lys Arg Gly Asn Phe Thr Ala Asp Glu Gln Leu Leu Ile Leu  
85 90 95

Asp Leu His Ser Arg Trp Gly Asn Arg Trp Ser Lys Xaa Ala Xaa His  
100 105 110

Leu Pro Gly Arg Thr Asp Asn Glu Asp Xaa Arg Thr Thr Gly Arg Thr  
115 120 125

Xaa Val Gln  
130

<210> 61  
<211> 464  
<212> DNA  
<213> Triticum aestivum

<220>  
<221> unsure  
<222> (435)

<220>  
<221> unsure  
<222> (442)

<220>  
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<222> (450)

<220>  
<221> unsure  
<222> (457)

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ggcaactggc gcgccgtccc caccaggacc ggctgatgc ggtgtagcaa gagctgccgg 180  
ctccggtgga ccaactacct gcgcccaggg atcaagcgcg gcaacttcac cgaccaggag 240  
gagaagctca tcgtccacct ccaggcgctg ctcggaaca ggtgggocgc gatcgctcc 300  
tacctccccg agcgcaccga caacgacatc aagaactact ggaacacgca actcaagcgc 360  
aagctgcaag cggggggcga cgccgcgggc aaaccggcgg cgcaaaggct gctcctcctc 420  
aaagggcaat ggganaggcg gngcagacgn catcaanatg cgcc 464

<210> 62  
<211> 122  
<212> PRT  
<213> Triticum aestivum

<400> 62  
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 Trp Thr Pro Glu Glu Asp Leu Val Leu Val Ser Tyr Val Gln Glu His  
 20 25 30  
 Gly Pro Gly Asn Trp Arg Ala Val Pro Thr Arg Thr Gly Leu Met Arg  
 35 40 45  
 Cys Ser Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Gly  
 50 55 60  
 Ile Lys Arg Gly Asn Phe Thr Asp Gln Glu Glu Lys Leu Ile Val His  
 65 70 75 80  
 Leu Gln Ala Leu Leu Gly Asn Arg Trp Ala Ala Ile Ala Ser Tyr Leu  
 85 90 95  
 Pro Glu Arg Thr Asp Asn Asp Ile Lys Asn Tyr Trp Asn Thr Gln Leu  
 100 105 110  
 Lys Arg Lys Leu Gln Ala Gly Gly Asp Ala  
 115 120  
 <210> 63  
 <211> 217  
 <212> PRT  
 <213> Pisum sativum  
 <400> 63  
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 Gly Pro Trp Thr Met Glu Glu Asp Leu Ile Leu Ile Asn Tyr Ile Ala  
 20 25 30  
 Asn His Gly Glu Gly Val Trp Asn Ser Leu Ala Lys Ala Ala Gly Leu  
 35 40 45  
 Lys Arg Thr Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg  
 50 55 60  
 Pro Asp Val Arg Arg Gly Asn Ile Thr Pro Glu Glu Gln Leu Leu Ile  
 65 70 75 80  
 Met Glu Leu His Ser Lys Trp Gly Asn Arg Trp Ser Lys Ile Ala Lys  
 85 90 95  
 His Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Phe Trp Arg Thr  
 100 105 110  
 Arg Ile Gln Lys His Ile Lys Gln Val Asp Asn Pro Asn Gln Gln Asn  
 115 120 125  
 Phe Gln Gln Lys Met Ser Leu Glu Ile Asn Asp His His His His His  
 130 135 140

Pro His Gln Pro Ser Ser Ser Gln Val Ser Asn Leu Val Glu Pro Met  
 145 150 155 160

Glu Thr Tyr Ser Pro Thr Ser Tyr Gln Gly Thr Leu Glu Pro Phe Pro  
 165 170 175

Thr Gln Phe Pro Thr Ile Asn Asn Asp His His Gln Asn Ser Asn Cys  
 180 185 190

Cys Ala Asn Asp Asn Asn Asn Asn Asn Tyr Trp Ser Met Glu Asp Ile  
 195 200 205

Trp Ser Met Gln Leu Leu Asn Gly Asp  
 210 215

100151121101